

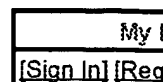
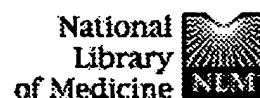
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6	BRS	L6	26	ipns[TI]
7	BRS	L7	124	synthetases near10 isopenicillin
8	BRS	L8	0	l7 near10 "212"
9	BRS	L9	8	l7 near10 (variant or mutant or modified)

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FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 08:40:12 ON 01 SEP 2005

L1	520 S ISOPENICILLIN (2N) SYNTHETASE
L2	160 S L1 AND (MUTA? OR VAR? OR MODI?)
L3	105 DUP REM L2 (55 DUPLICATES REMOVED)
L4	39 S L3 AND NIDULANS
L5	4 S L4 AND (212 OR ARG OR ARGININE)
L6	0 S L4 AND (212 OR GLU OR GLUTAMIC)
L7	8 S L4 AND E
L8	8 DUP REM L7 (0 DUPLICATES REMOVED)

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#6	Search 1.21.3.1[EC/RN Number] and mutant	08:45:05	28
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Search for

NiceZyme View of ENZYME: EC 1.21.3.1

Official Name

Isopenicillin-N synthase.

Reaction catalysed

N-((5S)-5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine + O(2) <=> isopenicillin N + 2 H(2)O

Comment(s)

Forms part of the penicillin biosynthesis pathway.

Cross-references

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PUMA2 [1.21.3.1](#)

PRIAM enzyme-specific profiles [1.21.3.1](#)

Kyoto University LIGAND chemical database [1.21.3.1](#)

IUBMB Enzyme Nomenclature [1.21.3.1](#)

IntEnz [1.21.3.1](#)

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☐ 1: Biophys Chem. 2000 Aug 30;86(2-3):109-18.

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Structure-function studies of the non-heme iron active site of isopenicillin N synthase: some implications for catalysis.

Kreisberg-Zakarin R, Borovok I, Yanko M, Frolow F, Aharonowitz Y, Cohen G.

Department of Molecular Microbiology and Biotechnology, The George S. Wise Faculty of Life Sciences, Tel Aviv University, Ramat Aviv, Israel.

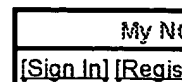
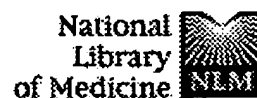
Isopenicillin N synthase (IPNS) is a non-heme ferrous iron-dependent oxygenase that catalyzes the ring closure of delta-(L-alpha-aminoadipoyl)-L-cysteinyl-D-valine (ACV) to form isopenicillin N. Spectroscopic studies and the crystal structure of IPNS show that the iron atom in the active species is coordinated to two histidine and one aspartic acid residues, and to ACV, dioxygen and H₂O. We previously showed by site-directed mutagenesis that residues His212, Asp214 and His268 in the IPNS of *Streptomyces jumonjinensis* are essential for activity and correspond to the iron ligands identified by crystallography. To evaluate the importance of the nature of the protein ligands for activity, His214 and His268 were exchanged with asparagine, aspartic acid and glutamine, and Asp214 replaced with glutamic acid, histidine and cysteine, each of which has the potential to bind iron. Only the Asp214Glu mutant retained activity, approximately 1% that of the wild type. To determine the importance of the spatial arrangement of the protein ligands for activity, His212 and His268 were separately exchanged with Asp214; both mutant enzymes were completely defective. These findings establish that IPNS activity depends critically on the presence of two histidine and one carboxylate ligands in a unique spatial arrangement within the active site. Molecular modeling studies of the active site employing the *S. jumonjinensis* IPNS crystal structure support this view. Measurements of iron binding by the wild type and the Asp214Glu, Asp214His and Asp214Cys-modified proteins suggest that Asp214 may have a role in catalysis as well as in iron coordination.

PMID: 11026676 [PubMed - indexed for MEDLINE]

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☐ 1: [Loke P, Sim TS.](#)[Related Articles, Links](#)

Mutational evidence for the role of serine-283 in Cephalosporium acremonium isopenicillin N synthase.

FEMS Microbiol Lett. 1998 Aug 15;165(2):353-6.

PMID: 9841222 [PubMed - indexed for MEDLINE]

☐ 2: [Loke P, Sim T.](#)[Related Articles, Links](#)

Site-directed mutagenesis of arginine-89 supports the role of its guanidino side-chain in substrate binding by Cephalosporium acremonium isopenicillin N synthase.

FEMS Microbiol Lett. 1999 Oct 15;179(2):423-9.

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☐ 3: [Loke P, Sim TS.](#)[Related Articles, Links](#)

Mutational analysis of tyrosine-191 in the catalysis of Cephalosporium acremonium isopenicillin N synthase.

J Biochem (Tokyo). 2000 Apr;127(4):585-9.

PMID: 10739949 [PubMed - indexed for MEDLINE]

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Functional analysis of a conserved aspartate D218 in Cephalosporium acremonium isopenicillin N synthase.

FEMS Microbiol Lett. 1997 Dec 1;157(1):137-40.

PMID: 9418249 [PubMed - indexed for MEDLINE]

☐ 5: [Loke P, Sim TS.](#)[Related Articles, Links](#)

Mutational analysis of conserved glycines 42 and 256 in Cephalosporium acremonium isopenicillin N synthase.

Can J Microbiol. 2001 Oct;47(10):961-4.

PMID: 11718551 [PubMed - indexed for MEDLINE]









☐ 6: [Loke P, Sim TS.](#)[Related Articles, Links](#)


Site-directed mutagenesis of proline-285 to leucine in Cephalosporium acremonium isopenicillin-N-synthase affects catalysis and increases soluble expression at higher temperatures.

Z Naturforsch [C]. 2001 May-Jun;56(5-6):413-5.

PMID: 11421458 [PubMed - indexed for MEDLINE]


☐ 7: [Loke P, Sim TS.](#)[Related Articles, Links](#)

-  **Analysis of glutamines in catalysis in *Cephalosporium acremonium* isopenicillin N synthase by site-directed mutagenesis.**
Biochem Biophys Res Commun. 1998 Nov 18;252(2):472-5.
PMID: 9826554 [PubMed - indexed for MEDLINE]
- ☐ **8:** [Orville AM, Chen VJ, Kriauciunas A, Harpel MR, Fox BG, Munck E, Lipscomb JD](#) [Related Articles, Links](#)
-  **Thiolate ligation of the active site Fe²⁺ of isopenicillin N synthase derives from substrate rather than endogenous cysteine: spectroscopic studies of site-specific Cys----Ser mutated enzymes.**
Biochemistry. 1992 May 19;31(19):4602-12.
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- ☐ **9:** [Loke P, Sim TS](#) [Related Articles, Links](#)
-  **Catalytic activity in *Cephalosporium acremonium* isopenicillin N synthase does not involve glutamine-234.**
Biochem Biophys Res Commun. 1998 Jul 30;248(3):559-61.
PMID: 9703965 [PubMed - indexed for MEDLINE]
- ☐ **10:** [Loke P, Sim TS](#) [Related Articles, Links](#)
-  **Glutamine-230 influences enzyme solubility but not catalysis in *Streptomyces clavuligerus* isopenicillin N synthase.**
FEMS Microbiol Lett. 1999 Apr 15;173(2):439-43.
PMID: 10227172 [PubMed - indexed for MEDLINE]
- ☐ **11:** [Tiow-Suan S, Tan DS](#) [Related Articles, Links](#)
-  **Histidine-272 of isopenicillin N synthase of *Cephalosporium acremonium*, which is possibly involved in iron binding, is essential for its catalytic activity.**
FEMS Microbiol Lett. 1994 Jul 15;120(3):241-7.
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- ☐ **12:** [Tan DS, Sim TS](#) [Related Articles, Links](#)
-  **Functional analysis of conserved histidine residues in *Cephalosporium acremonium* isopenicillin N synthase by site-directed mutagenesis.**
J Biol Chem. 1996 Jan 12;271(2):889-94.
PMID: 8557701 [PubMed - indexed for MEDLINE]
- ☐ **13:** [Borovok I, Landman O, Kreisberg-Zakarin R, Aharonowitz Y, Cohen G](#) [Related Articles, Links](#)
-  **Ferrous active site of isopenicillin N synthase: genetic and sequence analysis of the endogenous ligands.**
Biochemistry. 1996 Feb 13;35(6):1981-7.
PMID: 8639682 [PubMed - indexed for MEDLINE]
- ☐ **14:** [Loke P, Sim TS](#) [Related Articles, Links](#)
-  **Replacement of tyrosine-197 and the corresponding tyrosine-195 to isoleucine in *Cephalosporium acremonium* and *Streptomyces clavuligerus* isopenicillin N synthase.**
Z Naturforsch [C]. 2001 Sep-Oct;56(9-10):806-9.
PMID: 11724386 [PubMed - indexed for MEDLINE]
- ☐ **15:** [Scott RA, Wang S, Eidsness MK, Kriauciunas A, Frolik CA, Chen VJ](#) [Related Articles, Links](#)
- X-ray absorption spectroscopic studies of the high-spin iron(II) active site**


-  of isopenicillin N synthase: evidence for Fe-S interaction in the enzyme-substrate complex.


Biochemistry. 1992 May 19;31(19):4596-601.
PMID: 1581312 [PubMed - indexed for MEDLINE]

-  **16:** [Long AJ, Clifton LJ, Roach PL, Baldwin JE, Rutledge PJ, Schofield CJ.](#) [Related Articles, Links](#)


-  Structural studies on the reaction of isopenicillin N synthase with the truncated substrate analogues delta-(L-alpha-aminoadipoyl)-L-cysteinyl-glycine and delta-(L-alpha-aminoadipoyl)-L-cysteinyl-D-alanine.


Biochemistry. 2005 May 3;44(17):6619-28.
PMID: 15850395 [PubMed - indexed for MEDLINE]

-  **17:** [Blackburn JM, Sutherland JD, Baldwin JE.](#) [Related Articles, Links](#)

-  A heuristic approach to the analysis of enzymic catalysis: reaction of delta-(L-alpha-aminoadipoyl)-L-cysteinyl-D-alpha-aminobutyrate and delta-(L-alpha-aminoadipoyl)-L-cysteinyl-D-allylglycine catalyzed by isopenicillin N synthase isozymes.


Biochemistry. 1995 Jun 6;34(22):7548-62.
PMID: 7779800 [PubMed - indexed for MEDLINE]

-  **18:** [Kreisberg-Zakarin R, Borovok I, Yanko M, Frolov F, Aharonowitz Y, Cohen G.](#) [Related Articles, Links](#)


-  Structure-function studies of the non-heme iron active site of isopenicillin N synthase: some implications for catalysis.


Biophys Chem. 2000 Aug 30;86(2-3):109-18.
PMID: 11026676 [PubMed - indexed for MEDLINE]

-  **19:** [Tan DS, Ang SG, Sim TS.](#) [Related Articles, Links](#)

-  Involvement of a third histidine in the ferrous active site of isopenicillin N synthase of Cephalosporium acremonium repudiated by recombinant double histidine mutants.

Biochem Mol Biol Int. 1998 Feb;44(2):333-45.
PMID: 9530516 [PubMed - indexed for MEDLINE]

-  **20:** [Chen VJ, Orville AM, Harpel MR, Frolik CA, Surerus KK, Munck E, Lipscomb JD.](#) [Related Articles, Links](#)

-  Spectroscopic studies of isopenicillin N synthase. A mononuclear nonheme Fe²⁺ oxidase with metal coordination sites for small molecules and substrate.

J Biol Chem. 1989 Dec 25;264(36):21677-81.
PMID: 2557336 [PubMed - indexed for MEDLINE]

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RESULT 1

IPNS_EMENI

ID IPNS_EMENI STANDARD; PRT; 331 AA.

AC P05326;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N synthase).

GN Name=IPNA; Synonyms=IPS;

OS Emericella nidulans (*Aspergillus nidulans*).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; Emericella.

OX NCBI_TaxID=162425;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=88084424; PubMed=3319778; DOI=10.1016/0378-1119(87)90120-X;

RA Ramon D., Carramolino L., Patino C., Sanchez F., Penalva M.A.;

RT "Cloning and characterization of the isopenicillin N synthetase gene

RT mediating the formation of the beta-lactam ring in *Aspergillus*

RT *nidulans*.";

RL Gene 57:171-181(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=88314868; PubMed=3045077;

RA Weigel B.J., Burgett S.G., Chen V.J., Skatrud P.L., Frolik C.A.,

RA Queener S.W., Ingolia T.D.;

RT "Cloning and expression in *Escherichia coli* of isopenicillin N

RT synthetase genes from *Streptomyces lipmanii* and *Aspergillus*

RT *nidulans*.";

RL J. Bacteriol. 170:3817-3826(1988).

RN [3]

RP CRYSTALLIZATION.

RX MEDLINE=95392381; PubMed=7663335;

RA Roach P.L., Schofield C.J., Baldwin J.E., Clifton I.J., Hajdu J.;

RT "Crystallization and preliminary X-ray diffraction studies on

RT recombinant isopenicillin N synthase from *Aspergillus nidulans*.";

RL Protein Sci. 4:1007-1009(1995).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

RX MEDLINE=95312111; PubMed=7791906; DOI=10.1038/375700a0;

RA Roach P.L., Clifton I.J., Fueloep V., Harlos K., Barton G.J.,

RA Hajdu J., Andersson I., Schofield C.J., Baldwin J.E.;

RT "Crystal structure of isopenicillin N synthase is the first from a new

RT structural family of enzymes.";

RL Nature 375:700-704(1995).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).

RX MEDLINE=97337872; PubMed=9194566; DOI=10.1038/42990;

RA Roach P.L., Clifton I.J., Hensgens C.M., Shibata N., Schofield C.J.,

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RT "Structure of isopenicillin N synthase complexed with substrate and

RT the mechanism of penicillin formation.";

RL Nature 387:827-830(1997).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).

RX MEDLINE=20005505; PubMed=10537113; DOI=10.1038/44400;

RA Burzlaff N.I., Rutledge P.J., Clifton I.J., Hensgens C.M.H.,
 RA Pickford M., Adlington R.M., Roach P.L., Baldwin J.E.;
 RT "The reaction cycle of isopenicillin N synthase observed by X-ray
 RT diffraction.";
 RL Nature 401:721-724(1999).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.3 ANGSTROMS).
 RX MEDLINE=21628900; PubMed=11755401; DOI=10.1016/S1074-5521(01)00090-4;
 RA Ogle J.M., Clifton I.J., Rutledge P.J., Elkins J.M., Burzlaff N.I.,
 RA Adlington R.M., Roach P.L., Baldwin J.E.;
 RT "Alternative oxidation by isopenicillin N synthase observed by X-ray
 RT diffraction.";
 RL Chem. Biol. 8:1231-1237(2001).
 CC -!- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms
 CC from delta-L-(alpha-aminoadipyl)-L-cysteinyl-D-valine (ACV) to
 CC form the azetidinone and thiazolidine rings of isopenicillin.
 CC -!- CATALYTIC ACTIVITY: N-[(5S)-5-amino-5-carboxypentanoyl]-L-
 CC cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
 CC -!- COFACTOR: Iron and ascorbate.
 CC -!- PATHWAY: Biosynthesis of penicillin and cephalosporin.
 CC -!- SIMILARITY: Belongs to the iron/ascorbate-dependent oxidoreductase
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 DR PDB; 1QJF; X-ray; A=1-331.
 DR InterPro; IPR005123; 2OG-FeII_Oxy.
 DR InterPro; IPR002283; IPN_synth.
 DR InterPro; IPR002057; Isopen_N_synth.
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 DR PRINTS; PR00682; IPNSYNTHASE.
 DR PROSITE; PS00185; IPNS_1; 1.
 DR PROSITE; PS00186; IPNS_2; 1.
 KW 3D-structure; Antibiotic biosynthesis; Iron; Oxidoreductase;

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FT	STRAND	101	105	
FT	TURN	108	109	
FT	TURN	112	113	
FT	HELIX	115	118	
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FT	TURN	246	247	
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FT	HELIX	255	260	
FT	TURN	261	263	
FT	STRAND	270	273	
FT	STRAND	279	286	
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SQ	SEQUENCE	331 AA;	37522 MW;	5BA1A726E9EEFA25 CRC64;

Query Match

99.7%; Score 1766; DB 1; Length 331;

Best Local Similarity 99.7%; Pred. No. 7.5e-141;
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Db      1 MGSVSKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRD TGFFYAVNHGINVQRLSQKTKE 60

Qy     61 FHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAK 120
        |||||||||||||||||||||||||||||||||||||||
Db     61 FHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAK 120

Qy    121 TPTHEVNVWPDETKHPGFQDFAEQYYWDVFG LSSALLKGYALALGKEENFFARHFKPDDT 180
        |||||||||||||||||||||||||||||||||||||||
Db    121 TPTHEVNVWPDETKHPGFQDFAEQYYWDVFG LSSALLKGYALALGKEENFFARHFKPDDT 180

Qy    181 LASVVLIRYPYLDPYPEAAIKTAADG TKLSFRWHEDVSLITVLYQSNVQNLQVETAAGYQ 240
        |||||||||||||||||||||||||||||||||||||||
Db    181 LASVVLIRYPYLDPYPEAAIKTAADG TKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQ 240

Qy    241 DIEADDTGYLINCGSYMAHLTN NYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPR 300
        |||||||||||||||||||||||||||||||||||||||
Db    241 DIEADDTGYLINCGSYMAHLTN NYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPR 300

Qy    301 EPNGKSDREPLSYGDY LQNGLVSLINKNGQT 331
        |||||||||||||||||||||||||||
Db    301 EPNGKSDREPLSYGDY LQNGLVSLINKNGQT 331
```

RESULT 1

A27355

isopenicillin N synthase (EC 1.14.11.-) IPS [similarity] - Emericella nidulans

C;Species: Emericella nidulans, Aspergillus nidulans

C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004

C;Accession: A27355; A32344

R;Ramon, D.; Carramolino, L.; Patino, C.; Sanchez, F.; Penalva, M.A.

Gene 57, 171-181, 1987

A;Title: Cloning and characterization of the isopenicillin N synthetase gene mediating the formation of the beta-lactam ring in Aspergillus nidulans.

A;Reference number: A27355; MUID:88084424; PMID:3319778

A;Accession: A27355

A;Molecule type: DNA

A;Residues: 1-331 <RAM>

A;Cross-references: UNIPROT:P05326; GB:M18111; NID:g168056; PIDN:AAA33311.1; PID:g168057

R;Weigel, B.J.; Burgett, S.G.; Chen, V.J.; Skatrud, P.L.; Frolik, C.A.; Queener, S.W.; Ingolia, T.D.

J. Bacteriol. 170, 3817-3826, 1988

A;Title: Cloning and expression in Escherichia coli of isopenicillin N synthetase genes from Streptomyces lipmanii and Aspergillus nidulans.

A;Reference number: A91881; MUID:88314868; PMID:3045077

A;Accession: A32344

A;Molecule type: DNA

A;Residues: 1-331 <WEI>

A;Cross-references: GB:M21882; NID:g168054; PIDN:AAA33310.1; PID:g168055

C;Genetics:

A;Gene: IPS

C;Superfamily: isopenicillin N synthase

C;Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase

F;47,214,270/Binding site: iron (His) #status predicted

Query Match 99.7%; Score 1766; DB 2; Length 331;

Best Local Similarity 99.7%; Pred. No. 1.9e-142;

Matches 330; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSVSKANVPKIDVSPFLFGDDQAAMRVAQQIDAASRD TGFFYAVNHGINVQRLSQKTKE 60
 |||

Db 1 MGSVSKANVPKIDVSPFLFGDDQAAMRVAQQIDAASRD TGFFYAVNHGINVQRLSQKTKE 60

Qy 61 FHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAK 120
 |||

Db 61 FHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAK 120

Qy 121 TPTHEVNVWPDETKHPGFQDFAEQYYWDVFG LSSALLKGYALALGKEENFFARHFKPDDT 180
 |||

Db 121 TPTHEVNVWPDETKHPGFQDFAEQYYWDVFG LSSALLKGYALALGKEENFFARHFKPDDT 180

Qy 181 LASVVLIRYPYLDPYPEAAIKTAADGTKLSFRWHEDVSLITVLYQSNVQNLQVETAAGYQ 240
 |||

Db 181 LASVVLIRYPYLDPYPEAAIKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQ 240

Qy 241 DIEADDTGYLINCGSYMAHLTNYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPR 300
 |||

Db 241 DIEADDTGYLINCGSYMAHLTNYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPR 300

Qy 301 EPNGKSDREPLSYGDYLQNGLVSLINKNGQT 331
|||||
Db 301 EPNGKSDREPLSYGDYLQNGLVSLINKNGQT 331

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1766	99.7	331	1	IPNS_EMENI	P05326 emericella
2	1468	82.9	331	1	IPNS_PENCH	P08703 penicillium
3	1350.5	76.3	338	1	IPNS_CEPAC	P05189 cephalospor
4	1308	73.9	331	2	Q9C1G1	Q9c1g1 kallichroma
5	1041	58.8	328	1	IPNS_NOCLA	P27744 nocardia la
6	1015.5	57.3	331	2	Q9LCZ2	Q9lcz2 streptomyce
7	1014.5	57.3	329	1	IPNS_STRJU	P18286 streptomyce
8	1005.5	56.8	329	2	Q9ANU0	Q9anu0 streptomyce
9	993.5	56.1	326	1	IPNS_LYSLA	Q48739 lysobacter
10	986.5	55.7	329	1	IPNS_STRCL	P10621 streptomyce
11	985.5	55.6	326	1	IPNS_FLASS	P16020 flavobacter
12	985.5	55.6	329	1	IPNS_STRGR	Q54243 streptomyce
13	980.5	55.4	333	1	IPNS_STRLP	P12438 streptomyce
14	843.5	47.6	262	2	Q9FAB6	Q9fab6 streptomyce
15	837.5	47.3	262	2	Q9FAC2	Q9fac2 streptomyce
16	830.5	46.9	262	2	Q9FAB8	Q9fab8 streptomyce
17	825.5	46.6	262	2	Q9FAC1	Q9fac1 streptomyce
18	823.5	46.5	262	2	Q9FAB9	Q9fab9 streptomyce
19	822.5	46.4	262	2	Q9FAC0	Q9fac0 streptomyce
20	819.5	46.3	262	2	Q9FAC3	Q9fac3 streptomyce
21	800.5	45.2	262	2	Q9FAB7	Q9fab7 streptomyce
22	738.5	41.7	321	1	IPNS_STRCT	Q53932 streptomyce
23	685.5	38.7	221	2	Q9F5K9	Q9f5k9 streptomyce
24	405	22.9	237	2	Q9X6N2	Q9x6n2 streptomyce
25	357.5	20.2	319	2	Q7YUI1	Q7yui1 trypanosoma
26	348.5	19.7	319	2	Q7YUH6	Q7yuh6 trypanosoma

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1771	100.0	331	4	AAE12000	Aae12000 Aspergill
2	1771	100.0	331	4	AAE12001	Aae12001 Aspergill
3	1771	100.0	331	4	AAE12002	Aae12002 Aspergill
4	1771	100.0	331	6	ABG73754	Abg73754 E. nidula
5	1771	100.0	331	6	ABG73755	Abg73755 E. nidula
6	1771	100.0	331	6	ABG73753	Abg73753 E. nidula
7	1766	99.7	331	1	AAP80427	Aap80427 Sequence
8	1764	99.6	331	2	AAW63751	Aaw63751 A. nidula
9	1762	99.5	331	2	AAW63749	Aaw63749 A. nidula
10	1761	99.4	331	1	AAP93353	Aap93353 Aspergill
11	1754	99.0	331	8	ADS24092	Ads24092 Bacterial
12	1751	98.9	331	2	AAW63750	Aaw63750 A. nidula
13	1584	89.4	331	2	AAW63752	Aaw63752 A. nidula
14	1473	83.2	331	4	AAE12003	Aae12003 Penicilli
15	1473	83.2	331	6	ABG73756	Abg73756 P. chryso
16	1463	82.6	331	1	AAP70167	Aap70167 Sequence
17	1363.5	77.0	338	4	AAE12006	Aae12006 Acremoniu
18	1363.5	77.0	338	6	ABG73759	Abg73759 A. chryso
19	1355.5	76.5	338	4	AAE12005	Aae12005 Acremoniu
20	1355.5	76.5	338	6	ABG73758	Abg73758 A. chryso
21	1350.5	76.3	339	1	AAP60508	Aap60508 Isopenici

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1771	100.0	331	3	US-09-413-231-1	Sequence 1, Appli
2	1771	100.0	331	3	US-09-413-231-2	Sequence 2, Appli
3	1771	100.0	331	3	US-09-413-231-3	Sequence 3, Appli
4	1473	83.2	331	3	US-09-413-231-4	Sequence 4, Appli
5	1363.5	77.0	338	3	US-09-413-231-7	Sequence 7, Appli
6	1355.5	76.5	338	3	US-09-413-231-6	Sequence 6, Appli
7	991.5	56.0	329	3	US-09-413-231-5	Sequence 5, Appli
8	991.5	56.0	329	3	US-09-413-231-9	Sequence 9, Appli
9	985.5	55.6	333	3	US-09-413-231-10	Sequence 10, Appl
10	743.5	42.0	321	3	US-09-413-231-8	Sequence 8, Appli
11	540	30.5	188	3	US-08-861-774E-16	Sequence 16, Appl
12	336	19.0	390	4	US-09-252-991A-20513	Sequence 20513, A

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1771	100.0	331	9	US-09-924-841-1	Sequence 1, Appli
2	1771	100.0	331	9	US-09-924-841-2	Sequence 2, Appli
3	1771	100.0	331	9	US-09-924-841-3	Sequence 3, Appli
4	1754	99.0	331	15	US-10-369-493-13125	Sequence 13125, A
5	1473	83.2	331	9	US-09-924-841-4	Sequence 4, Appli
6	1363.5	77.0	338	9	US-09-924-841-7	Sequence 7, Appli
7	1355.5	76.5	338	9	US-09-924-841-6	Sequence 6, Appli
8	991.5	56.0	329	9	US-09-924-841-5	Sequence 5, Appli
9	991.5	56.0	329	9	US-09-924-841-9	Sequence 9, Appli
10	985.5	55.6	333	9	US-09-924-841-10	Sequence 10, Appl
11	743.5	42.0	321	9	US-09-924-841-8	Sequence 8, Appli

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1766	99.7		331	2	A27355	isopenicillin N sy
2	1476	83.3		331	2	S04441	isopenicillin N sy
3	1468	82.9		331	2	A26467	isopenicillin N sy
4	1350.5	76.3		338	2	A24567	isopenicillin N sy
5	1350.5	76.3		338	2	S09312	isopenicillin N sy
6	1041	58.8		328	2	S15284	isopenicillin N sy
7	993.5	56.1		326	2	S54099	isopenicillin N sy
8	986.5	55.7		329	2	A29894	isopenicillin N sy
9	985.5	55.6		326	2	S08218	isopenicillin N sy
10	985.5	55.6		329	2	A61155	isopenicillin N sy
11	980.5	55.4		333	2	B32344	isopenicillin N sy
12	738.5	41.7		321	2	A58458	isopenicillin N sy
13	335	18.9		334	2	E83122	probable iron/asco
14	303	17.1		320	2	C83628	probable oxidoredu
15	246.5	13.9		329	2	G86472	probable hyoscyami
16	241	13.6		306	2	T45586	hypothetical prote
17	233	13.2		386	2	T09664	gibberellin 20-oxi
18	228	12.9		355	2	AG0160	probable iron/asco
19	228	12.9		377	2	T10222	gibberellin 20-oxi
20	226	12.8		386	2	T09675	probable gibberell
21	219	12.4		380	2	T48491	gibberellin 20-oxi
22	218.5	12.3		361	2	T06330	gibberellin 20-dio
23	218.5	12.3		380	2	T06439	gibberellin 20-dio
24	218	12.3		332	2	T46239	hypothetical prote
25	218	12.3		397	2	S45496	sexual differentia
26	216.5	12.2		365	2	T06991	gibberellin 20-dio